

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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**Title:** US-09-762-491-5  
**perfect score:** 1557  
**Sequence:** 1 atgtcgtgcgtcaaggatg.....ataatcatagcgaaataa 1557  
**Scoring table:** IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

\_arched: 383533 seqs, 122816752 residues  
Total number of hits satisfying chosen parameters: 767066

ALIGNMENT

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/pctodata/2/ina/5A_COMB.seq:*
2: /cgn2_5/pctodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/pctodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/pctodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/pctodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/pctodata/2/ina/backfiles1.seq:*

```

**Pred.** No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribution

PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score	Match	Length	DB	ID	Description	
1	1548	6	99.5	1557	3	US-09-329-418-2	
2	1548	6	99.5	1557	4	US-09-531-914-2	
3	1526	4	98.0	1873	3	US-09-329-418-1	
4	1526	4	98.0	1873	4	US-09-531-914-1	
5	96.8	6	6.2	3516	3	US-09-188-930-257	
6	79.6	5	1	1888	3	US-09-188-930-66	
7	56.2	3	1	1461	3	US-09-344-001-1	
8	53.4	3	1	2610	2	US-09-212-771-1	
9	53.4	3	1	2610	3	US-09-091-058-1	
10	52.6	3	1	4	US-09-099-094-1A-3	Sequence 2, Appl	
11	52.6	3	1	1931	3	US-09-019-942-2	Sequence 2, Appl
12	52.6	3	1	1931	4	US-09-099-041A-1	Sequence 1, Appl
13	52.6	3	1	2502	4	US-09-099-023-2	Sequence 2, Appl
14	49.6	3	1	843	3	US-08-888-4-29A-25	Sequence 25, Appl
15	48.6	3	1	2962	2	US-08-449-645A-10	Sequence 10, Appl
16	48.6	3	1	2962	2	US-08-702-367A-10	Sequence 10, Appl
17	48.6	3	1	2962	5	PCT-US95-04681-10	Sequence 10, Appl
18	48.4	3	1	3239	4	US-09-228-986-9	Sequence 9, Appl
19	48.4	3	1	3590	1	US-08-587-889-1	Sequence 1, Appl
20	48.4	3	1	3590	5	PCT-US96-00193-1	Sequence 1, Appl
21	47	3	0	722	4	US-08-998-416-800	Sequence 800, Appl
22	45.6	2	9	2268	1	US-08-444-005-14	Sequence 14, Appl
23	45.6	2	9	4594	4	US-09-442-100-7	Sequence 7, Appl
24	45	2	9	3505	1	US-07-660-465-1	Sequence 1, Appl
25	45	2	9	3592	2	US-08-469-37A-100	Sequence 100, Appl
26	44.2	2	8	3323	2	US-08-422-699A-10	Sequence 10, Appl
27	44.2	2	8	3323	2	US-08-422-706B-10	Sequence 10, Appl

Triling date June 10, 1999  
RESULT 1  
US-09-329418-2  
Sequence 2, Application US/09329418  
PATENT NO. 6096539  
GENERAL INFORMATION:  
APPLICANT: ZENECA Limited  
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS  
FILE REFERENCE: PHM.70536  
CURRENT APPLICATION NUMBER: US/09/329,418  
CURRENT FILING DATE: 1999-06-11 ✓  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 1557  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-09-329418-2

**BEST AVAILABLE COPY** US-09-762-

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## OM protein - protein search, using sw model

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Run on:

August 13, 2002, 21:14:38 ; Search time 24.14 Seconds  
 (without alignments)  
 525.140 Million cell updates/sec

Title:

US-09-762-491-6  
 2774

Perfect score:

1 MSCYKLLWPSGAPARPLVSIEE..... PKDPEAWSRPGQWYNHSGKZ 519

Scoring table:

BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched:

231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:

231628  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1:	/cgn2-6/podata/2/1aa/5A_COMB.pep:*
2:	/cgn2-6/podata/2/1aa/5B_COMB.pep:*
3:	/cgn2-6/podata/2/1aa/6A_COMB.pep:*
4:	/cgn2-6/podata/2/1aa/6B_COMB.pep:*
5:	/cgn2-6/podata/2/1aa/potus_COMB.pep:*
6:	/cgn2-6/podata/2/1aa/backfile1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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Result No.	Score	Query Match Length	DB ID	Description
1	2750	99.1	518	3 US-09-329418-3
2	2750	99.1	518	4 US-09-531914-3
3	2747	90.0	518	3 US-09-329418-5
4	2747	99.0	518	4 US-09-531914-5
5	2742	98.8	518	3 US-09-329418-4
6	2742	98.8	518	4 US-09-531914-4
7	2722	98.1	518	3 US-09-329418-9
8	2722	98.1	518	4 US-09-531914-9
9	2145.5	77.3	420	3 US-09-329418-8
10	2145.5	77.3	420	4 US-09-531914-8
11	1358	49.9	261	3 US-09-329418-6
12	1358	49.0	261	4 US-09-531914-6
13	1305	47.0	240	3 US-09-329418-7
14	1305	47.0	240	4 US-09-531914-7
15	445.5	16.1	656	1 US-08-444-005-15
16	445.5	16.1	656	4 US-09-069-023-28
17	423	67.1	409	1 US-09-13211-2
18	423	15.2	709	1 US-08-444-005-17
19	407	14.7	787	4 US-09-188-930-334
20	379	13.7	531	4 US-09-069-023-1
21	379	13.7	540	3 US-09-199-942-1
22	379	13.7	540	4 US-09-099-041A-2
23	379	13.7	540	4 US-09-069-023-27
24	377	13.6	536	4 US-09-188-930-185
25	376	13.6	300	4 US-09-099-041A-4
26	376	13.6	530	4 US-09-069-023-3
27	335.5	12.1	478	4 US-09-069-023-3

ALIGNMEN

RESULT 1  
US-09-329-418-3  
; Sequence 3, Application US/09329418  
; Patent No. 6096539  
; GENERAL INFORMATION:  
; APPLICANT: ZENECA Limited  
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS  
; FILE REFERENCE: PHM\_70536  
; CURRENT APPLICATION NUMBER: US/09/329,418  
; CURRENT FILING DATE: 1999-06-11  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-329-418-3

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RESULT 2

US-09-531-914-3

; Sequence 3, Application US/09531914

; Patent No. 6267956

GENERAL INFORMATION:

; APPLICANT: ZENECA Limited

; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS

; FILE REFERENCE: PHM\_7036

CURRENT APPLICATION NUMBER: US/09/531.914

CURRENT FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 09/329,418

PRIOR FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 518.

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-531-914-3

Query Match 99.1%; Score 2750; DB 4; Length 518;

Best Local Similarity 99.4%; Pred. No. 1.7e-210; Indels 0; Gaps 0; Matches 515; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSCVKLWPSGAPAPLVSIELENOELVKGDKGTVFRAQRKRGYDIAKIVNSKAISRE 60

Db 1 MSCVKLWPSGAPAPLVSIELENOELVKGDKGTVFRAQRKRGYDIAKIVNSKAISRE 60

QY 61 VKAMASLDNEFVRLEGVEKVNNDQDPKPALVYKFMENSLSGLQSCPRPWPLCRL 120

Db 61 VKAMASLDNEFVRLEGVEKVNNDQDPKPALVYKFMENSLSGLQSCPRPWPLCRL 120

QY 121 LKEVVLGMYLHDQNPVILHDLKPSNVLPDELUVKLADEFLSTFGQSOGTSGEPG 180

Db 121 LKEVVLGMYLHDQNPVILHDLKPSNVLPDELUVKLADEFLSTFGQSOGTSGEPG 180

QY 181 GTLGYLAPLFVNVRKASTASDVYSGILMWAVLAGREVELPTPSLVEAVCNRQRP 240

Db 181 GTLGYLAPLFVNVRKASTASDVYSGILMWAVLAGREVELPTPSLVEAVCNRQRP 240

QY 241 SLAEPIQAGPETPGEGIKELMQCLWSEEDKDRPFOECUPLKPTDEVOMVNMMNAVST 300

Db 241 SLAEPIQAGPETPGEGIKELMQCLWSEEDKDRPFOECUPLKPTDEVOMVNMMNAVST 300

QY 301 VKDFLSQKSSNRRESIPESQGGTEMGRRTIENQHSRNDVMSEWLNKLNLLEPPSS 360

Db 301 VKDFLSQKSSNRRESIPESQGGTEMGRRTIENQHSRNDVMSEWLNKLNLLEPPSS 360

QY 361 VPKKCPSLIKRSRAQEQQPAWTAGTSSPSMAQPOTPTESTRNQMPSPSTSTGPSPG 420

Db 361 VPKKCPSLIKRSRAQEQQPAWTAGTSSPSMAQPOTPTESTRNQMPSPSTSTGPSPG 420

QY 421 PRGNQGAERGMNNSCRTBPNPYGRPLUNIYNQSGVQGDNNLTMQTALPWLGA 480

Db 421 PRGNQGAERGMNNSCRTBPNPYGRPLUNIYNQSGVQGDNNLTMQTALPWLGA 480

RESULT 4

US-09-531-914-5

; Sequence 5, Application US/09531914

; Patent No. 6267956

GENERAL INFORMATION:

; APPLICANT: ZENECA Limited

; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS

; FILE REFERENCE: PHM\_7036

CURRENT APPLICATION NUMBER: US/09/531.914

CURRENT FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 09/329,418

PRIOR FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 518

TYPE: PRT

ORGANISM: Dartificial Sequence

FEATURE: OTHER INFORMATION: Dominant Negative Mutant Embodiment

US-09-329-418-5

Query Match 99.0%; Score 2747; DB 3; Length 518;

Best Local Similarity 99.2%; Pred. No. 2.9e-210; Indels 0; Gaps 0; Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSCVKLWPSGAPAPLVSIELENOELVKGDKGTVFRAQRKRGYDIAKIVNSKAISRE 60

Db 1 MSCVKLWPSGAPAPLVSIELENOELVKGDKGTVFRAQRKRGYDIAKIVNSKAISRE 60

QY 61 VKAMASLDNEFVRLEGVEKVNNDQDPKPALVYKFMENSLSGLQSCPRPWPLCRL 120

Db 61 VKAMASLDNEFVRLEGVEKVNNDQDPKPALVYKFMENSLSGLQSCPRPWPLCRL 120

QY 121 LKEVVLGMYLHDQNPVILHDLKPSNVLPDELUVKLADEFLSTFGQSOGTSGEPG 180

Db 121 LKEVVLGMYLHDQNPVILHDLKPSNVLPDELUVKLADEFLSTFGQSOGTSGEPG 180

QY 181 GTLGYLAPLFVNVRKASTASDVYSGILMWAVLAGREVELPTPSLVEAVCNRQRP 240

Db 181 GTLGYLAPLFVNVRKASTASDVYSGILMWAVLAGREVELPTPSLVEAVCNRQRP 240

QY 241 SLAEPIQAGPETPGEGIKELMQCLWSEEDKDRPFOECUPLKPTDEVOMVNMMNAVST 300

Db 241 SLAEPIQAGPETPGEGIKELMQCLWSEEDKDRPFOECUPLKPTDEVOMVNMMNAVST 300

QY 301 VKDFLSQKSSNRRESIPESQGGTEMGRRTIENQHSRNDVMSEWLNKLNLLEPPSS 360

Db 301 VKDFLSQKSSNRRESIPESQGGTEMGRRTIENQHSRNDVMSEWLNKLNLLEPPSS 360

QY 361 VPKKCPSLIKRSRAQEQQPAWTAGTSSPSMAQPOTPTESTRNQMPSPSTSTGPSPG 420

Db 361 VPKKCPSLIKRSRAQEQQPAWTAGTSSPSMAQPOTPTESTRNQMPSPSTSTGPSPG 420

QY 421 PRGNQGAERGMNNSCRTBPNPYGRPLUNIYNQSGVQGDNNLTMQTALPWLGA 480

Db 421 PRGNQGAERGMNNSCRTBPNPYGRPLUNIYNQSGVQGDNNLTMQTALPWLGA 480

QY 481 PSGKGRGLQHPPPVGSQEGPKPEAWSRPOGWYNHSGK 518

Db 481 PSGKGRGLQHPPPVGSQEGPKPEAWSRPOGWYNHSGK 518